AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions, and listings, of the claims in the application.

1. -2.   (*Canceled*)

3.   (*Previously presented*) A method in a computer system for generating a graphic display for visualization of gene expression in a molecular topography, comprising:

providing a first set of data, the data comprising gene expression measurements and descriptive information for a first plurality of polynucleotides;

defining an X-Y plane having a first axis corresponding to sequence identifiers and a second axis corresponding to polynucleotide sizes;

generating a first gene expression profile within the X-Y plane for the first plurality of polynucleotides , the first profile comprising a plurality of peaks with each peak corresponding to a polynucleotide, the peak defined by:

(i) a first value comprising a sequence identifier for the polynucleotide;

(ii) a second value comprising a measure of size of the polynucleotide, wherein an intersection between the first value and the second value defines a point within the X-Y plane; and

(iii) at the point, plotting along a Z-axis intersecting the X-Y plane a third value that is a measure of quantity of the polynucleotide;

wherein the plurality of peaks is generated for the first plurality of polynucleotides so that the graphic display comprises a molecular topography of gene expression.

4.-24. (*Canceled*)

25. (*Previously presented*) The method of claim 3, further comprising:

providing a second set of data comprising gene expression measurements and descriptive information for a second plurality of polynucleotides;

generating a second gene expression profile within the X-Y plane for the second plurality of polynucleotides;

comparing the first and second gene expression profiles to generate a differential gene expression profile;

wherein the graphic display comprises the molecular topography of differential gene expression.

26. (*Previously presented*) The method of claim 25, wherein one of the first and second sets of data corresponds to a reference sample and the other of the first and second sets of data corresponds to a test sample.

27. (*Currently amended*) The method of claim 26, wherein the differential gene expression profile is diagnostic of a condition or disease.

28. (*Previously presented*) The method of claim 3, further comprising:

providing a plurality of subsequent sets of data for the same or comparable sample as the first set of data in a temporal succession; and

generating and displaying gene expression profiles for each subsequent set of data to observe dynamic changes in gene expression over time.

29. (*Previously presented*) The method of claim 28, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

30. (*Previously presented*) The method of claim 28, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.

31. (*Previously presented*) The method of claim 25, further comprising:

providing a plurality of subsequent sets of data for the same or comparable sample as the first and second sets of data in a temporal succession; and

generating and displaying differential gene expression profiles for each subsequent set of data to observe dynamic changes in differential gene expression over time.

32. (*Previously presented*) The method of claim 31, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

33. (*Previously presented*) The method of claim 31, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.

34. (*Previously presented*) A method in a computer system for generating a graphic display for visualization of gene expression data, comprising:

providing a first set of data, the data comprising gene expression measurements and descriptive information for a first plurality of polynucleotides;

defining an X-Y plane having a first axis corresponding to sequence identifiers and a second axis corresponding to polynucleotide sizes;

plotting within the X-Y plane a plurality of points corresponding to the first plurality of polynucleotides according to their sequence identifiers and polynucleotide sizes; and

for each point within the plane, plotting along a Z-axis intersecting the X-Y plane a measured value corresponding to a quantity of mRNA produced for the polynucleotide plotted at the point so that a peak extending from the X-Y plane is generated;

wherein the graphic display comprises a three-dimensional plot representative of gene expression for the first plurality of polynucleotides.

35. (*Previously presented*) The method of claim 34, further comprising:

providing a second set of data comprising gene expression measurements and descriptive information for a second plurality of polynucleotides;

generating a second gene expression profile within the X-Y plane for the second plurality of polynucleotides;

comparing the first and second gene expression profiles to generate a differential gene expression profile;

wherein the graphic display comprises the molecular topography of differential gene expression.

36. (*Previously presented*) The method of claim 35, wherein one of the first and second sets of data corresponds to a reference sample and the other of the first and second sets of data corresponds to a test sample.

37. (*Currently amended*) The method of claim 36, wherein the differential gene expression profile is diagnostic of a condition or disease.

38. (*Previously presented*) The method of claim 34, further comprising:

providing a plurality of subsequent sets of data for the same or comparable sample as the first set of data in a temporal succession; and

generating and displaying gene expression profiles for each subsequent set of data to observe dynamic changes in gene expression over time.

39. (*Previously presented*) The method of claim 38, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

40. (*Previously presented*) The method of claim 38, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process.

41. (*Previously presented*) The method of claim 35, further comprising:

providing a plurality of subsequent sets of data for the same or comparable sample as the first and second sets of data in a temporal succession; and

generating and displaying differential gene expression profiles for each subsequent set of data to observe dynamic changes in differential gene expression over time.

42. (*Previously presented*) The method of claim 41, wherein the subsequent sets of data are taken from samples comprising cells undergoing one or more of growth, differentiation and division.

43. (*Previously presented*) The method of claim 41, wherein the subsequent sets of data are taken from samples comprising cells undergoing disease process and/or therapy.